AGCATCCTGA GTAATGAGTG GCCTGGGCCG GAGCAGGCGA GGTGGCCGGA GCCGTGTGGA 60

CCAGGAGGAG CGCTTTCCAC AGGGCCTGTG GACGGGGGTG GCTATGAGAT CCTGCCCCGA 120

AGAGCAGTAC TGGGATCCTC TGCTGGGTAC CTGCATGTCC TGCAAAACCA TTTGCAACCA 180

TCAGAGCCAG CGCACCTGTG CAGCCTTCTG CAGGTCACTC AGCTGCCGCA AGGAGCAACG 240

CAAGTTCTAT GACCATCTCC TGAGGGACTG CATCAGCTGT GCCTCCATCT GTGGACAGCA 300

CCCTAAGCAA TGTGCATACT TCTGTGAGAA CAAGCTCAGG AGCCCAGTGA ACCTTCCACC 360

AGAGCTCAGG AGACAGCGGA GTGGAGAAGT TGAAAACAAT TCAGACAACT CGGGAAGGTA 420

CCAAGGATTG GAGCACAGAG GCTCAGAAGC AAGTCCAGCT CTCCCGGGGC TGAAGCTGAG 480

TGCAGATCAG GTGGCCCTGG TCTACAGCAC GCTGGGGCTC TGCCTGTGTG CCGTCCTCTG 540

CTGCTTCCTG GTGGCGGTGG CCTGCTTCCT CAAGAAGAGG GGGGATCCCT GCTCCTGCCA 600

GCCCCGCTCA AGGCCCCGTC AAAGTCCGGC CAAGTCTTCC CAGGATCACG CGATGGAAGC 660

CGGCAGCCCT GTGAGCACAT CCCCCGAGCC AGTGGAGACC TGCAGCTTCT GCTTCCCTGA 720

GTGCAGGGCG CCCACGCAGG AGAGCGCAGT CACGCCTGGG ACCCCCGACC CCACTTGTGC 780

TGGAAGGTGG GGGTGCCACA CCAGGACCAC AGTCCTGCAG CCTTGCCCAC ACATCCCAGA 840

CAGTGGCCTT GGCATTGTGT GTGTGCCTGC CCAGGAGGGG GGCCCAGGTG CATAAATGGG 900

GGTCAGGGAG GGAAAGGAGG AGGGAGAGAG ATGGAGAGGA GGGGAGAGAG AAAGAGAGGT 960

GGGGAGAGGG GAGAGAGATA TGAGGAGAGA GAGACAGAGG AGGCAGAAAG GGAGAGAAAC 1020

AGAGGAGACA GAGAGGGAGA GAGAGACAGA GGGAGAGAGA GACAGAGGGG AAGAGAGGCA 1080

GAGAGGGAAA GAGGCAGAGA AGGAAAGAGA CAGGCAGAGA AGGAGAGAGG CAGAGAGGGA 1140

GAGAGGCAGA GAGGGAGAGA GGCAGAGAGA CAGAGAGGGA GAGAGGGACA GAGAGAGATA 1200

GAGCAGGAGG TCGGGGCACT CTGAGTCCCA GTTCCCAGTG CAGCTGTAGG TCGTCATCAC 1260

CTAACCACAC GTGCAATAAA GTCCTCGTGC CTGCTGCTCA CAGCCCCCGA GAGCCCCTCC 1320

TCCTGGAGAA TAAAACCTTT GGCAGCTGCC CTTCCTCAAA AAAAAAAAAA AAAAAAA 1377

FIGURE 1A

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1 5 10 15

Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
20 25 30

Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
35 40 45

Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
50 55 60

Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65 70 75 80

His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
85 90 95

Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100 105 110

Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
115 120 125

Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
130 135 140

Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145 150 155 160

Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
165 170 175

Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
180 185 190

Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
195 200 205

Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
210 215 220

Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
225 230 235 240

Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
245 250 255

Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
260 265 270

His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
275 280 285

Gly Gly Pro Gly Ala
290

FIGURE 1B

AGCAAGTTCA GCCTGGTTAA GTCCAAGCTG AATTCCGGTC AAAGTTCAAG
TAGTGATATG GATGACTCCA CAGAAAGGGA GCAGTCACGC CTTACTTCTT
GCCTTAAGAA AAGAGAAGAA ATGAAACTGA AGGAGTGTGT TTCCATCCTC
CCACGGAAGG AAAGCCCCTC TGTCCGATCC TCCAAAGACG GAAAGCTGCT
GGCTGCAACC TTGCTGCTGG CACTGCTGTC TTGCTGCCTC ACGGTGGTGT
CTTTCTACCA GGTGGCCGCC CTGCAAGGGG ACCTGGCCAG CCTCCGGGCA
GAGCTGCAGG GCCACCACGC GGAGAAGCTG CCAGCAGGAG CAGGAGCCCC
CAAGGCCGGC CTGGAGGAAG CTCCAGCTGT CACCGCGGGA CTGAAAATCT
TTGAACCACC AGCTCCAGGA GAAGGCAACT CCAGTCAGAA CAGCAGAAAT
AAGCGTGCCG TTCAGGGTCC AGAAGAAACA GTCACTCAAG ACTGCTTGCA
ACTGATTGCA GACAGTGAAA CACCAACTAT ACAAAAAGGA TCTTACACAT
TTGTTCCATG GCTTCTCAGC TTTAAAAGGG GAAGTGCCCT AGAAGAAAAA
GAGAATAAAA TATTGGTCAA AGAAACTGGT TACTTTTTTA TATATGGTCA
GGTTTTATAT ACTGATAAGA CCTACGCCAT GGGACATCTA ATTCAGAGGA
AGAAGGTCCA TGTCTTTGGG GATGAATTGA GTCTGGTGAC TTTGTTTCGA
TGTATTCAAA ATATGCCTGA AACACTACCC AATAATTCCT GCTATTCAGC
TGGCATTGCA AAACTGGAAG AAGGAGATGA ACTCCAACTT GCAATACCAA
GAGAAAATGC ACAAATATCA CTGGATGGAG ATGTCACATT TTTTGGTGCA
TTGAAACTGC TGTGACCTAC TTACACCATG TCTGTAGCTA TTTTCCTCCC
TTTCTCTGTA CCTCTAAGAA GAAAGAATCT AACTGAAAAT ACCAAAAAAA
AAAAAAAAAA AAAAAGATCT TTAATTAAGC GGCCGCAAGC TTATTCCCTT
TAGTGAG

FIGURE 2A

MDDSTEREQS RLTSCLKKRE EMKLKECVSI LPRKESPSVR SSKDGKLLAA
TLLLALLSCC LTVVSFYQVA ALQGDLASLR AELQGHHAEK LPAGAGAPKA
GLEEAPAVTA GLKIFEPPAP GEGNSSQNSR NKRAVQGPEE TVTQDCLQLI
ADSETPTIQK GSYTFVPWLL SFKRGSALEE KENKILVKET GYFFIYGQVL
YTDKTYAMGH LIQRKKVHVF GDELSLVTLF RCIQNMPETL PNNSCYSAGI
AKLEEGDELQ LAIPRENAQI SLDGDVTFFG ALKLL

FIGURE 2B

MARRLWILSL LAVTLTVALA APSQKSKRRT SSDRMKQIED KIEEILSKIY
HIENEIARIK KLIGERTRSG NSSQNSRNKR AVQGPEETVT QDCLQLIADS
ETPTIQKGSY TFVPWLLSFK RGSALEEKEN KILVKETGYF FIYGQVLYTD
KTYAMGHLIQ RKKVHVFGDE LSLVTLFRCI QNMPETLPNN SCYSAGIAKL
EEGDELQLAI PRENAQISLD GDVTFFGALK LL
(SEQ ID NO:3)

FIGURE 3

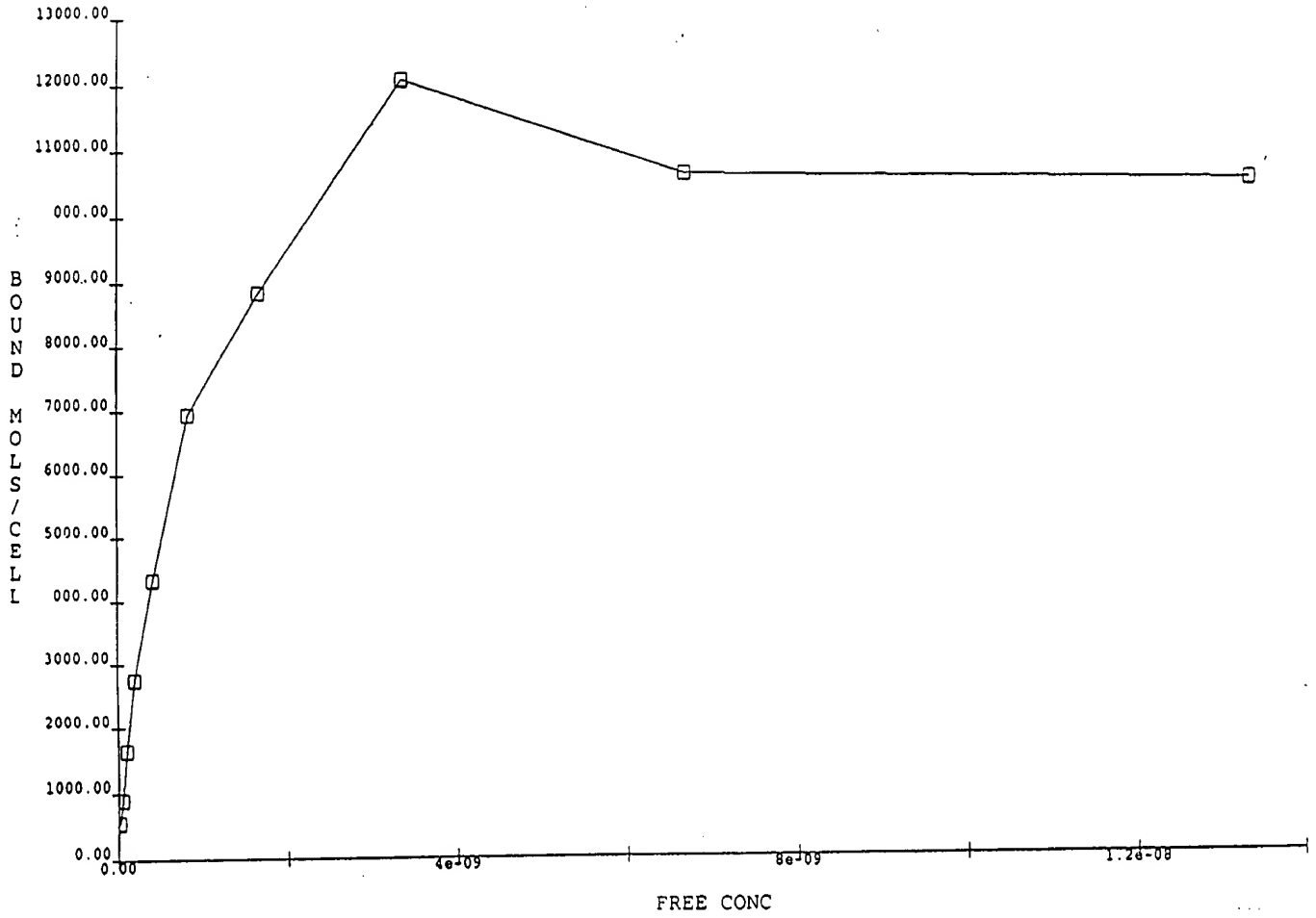
13000.00
12000.00
11000.00
000.00
9000.00
8000.00
7000.00
6000.00
5000.00
000.00
3000.00
2000.00
1000.00
0.00
BOUND MOLS/CELL
0.00
4e-09
8e-09
1.2e-08
FREE CONC

Figure 4A

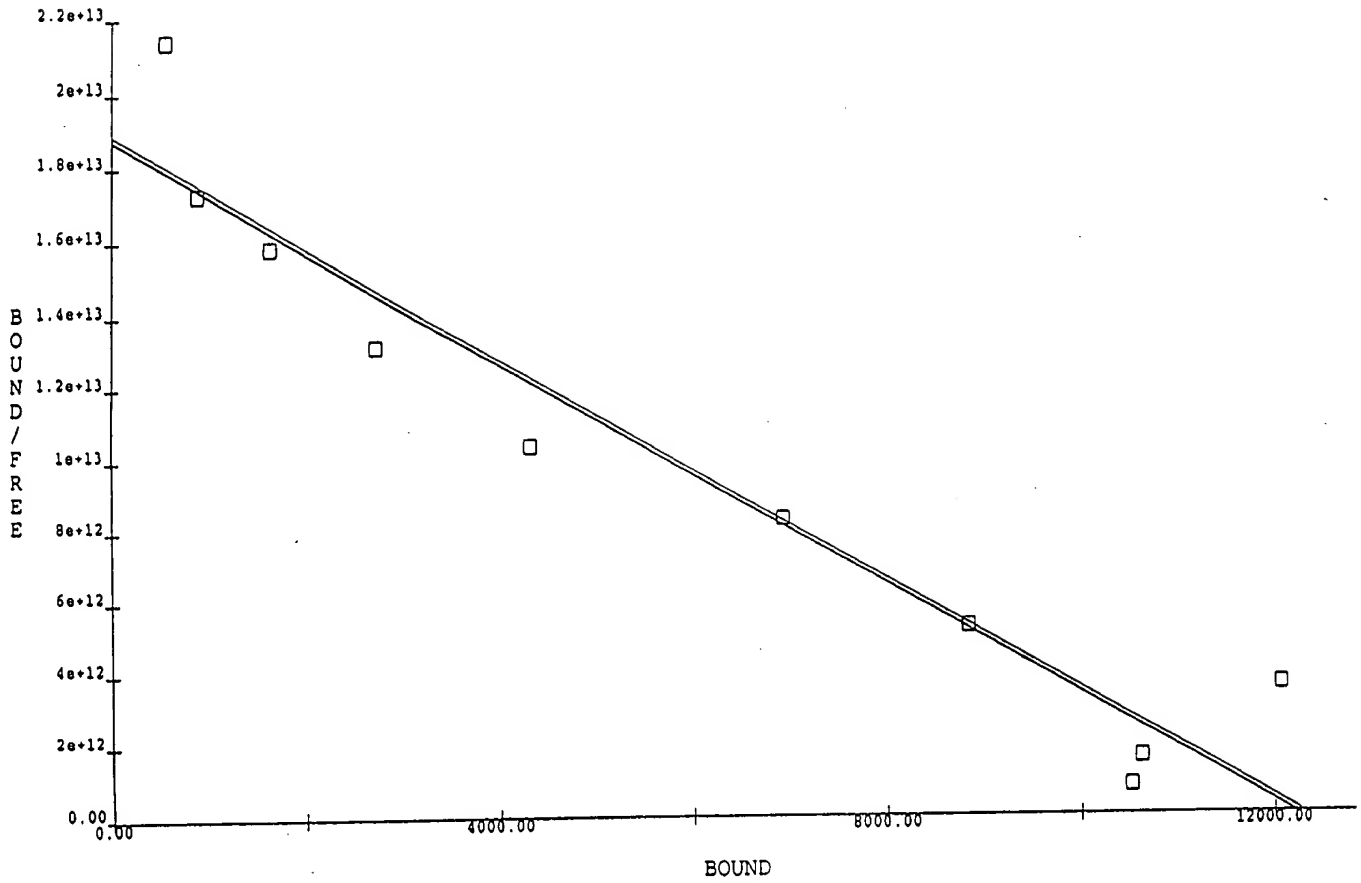

Figure 4B

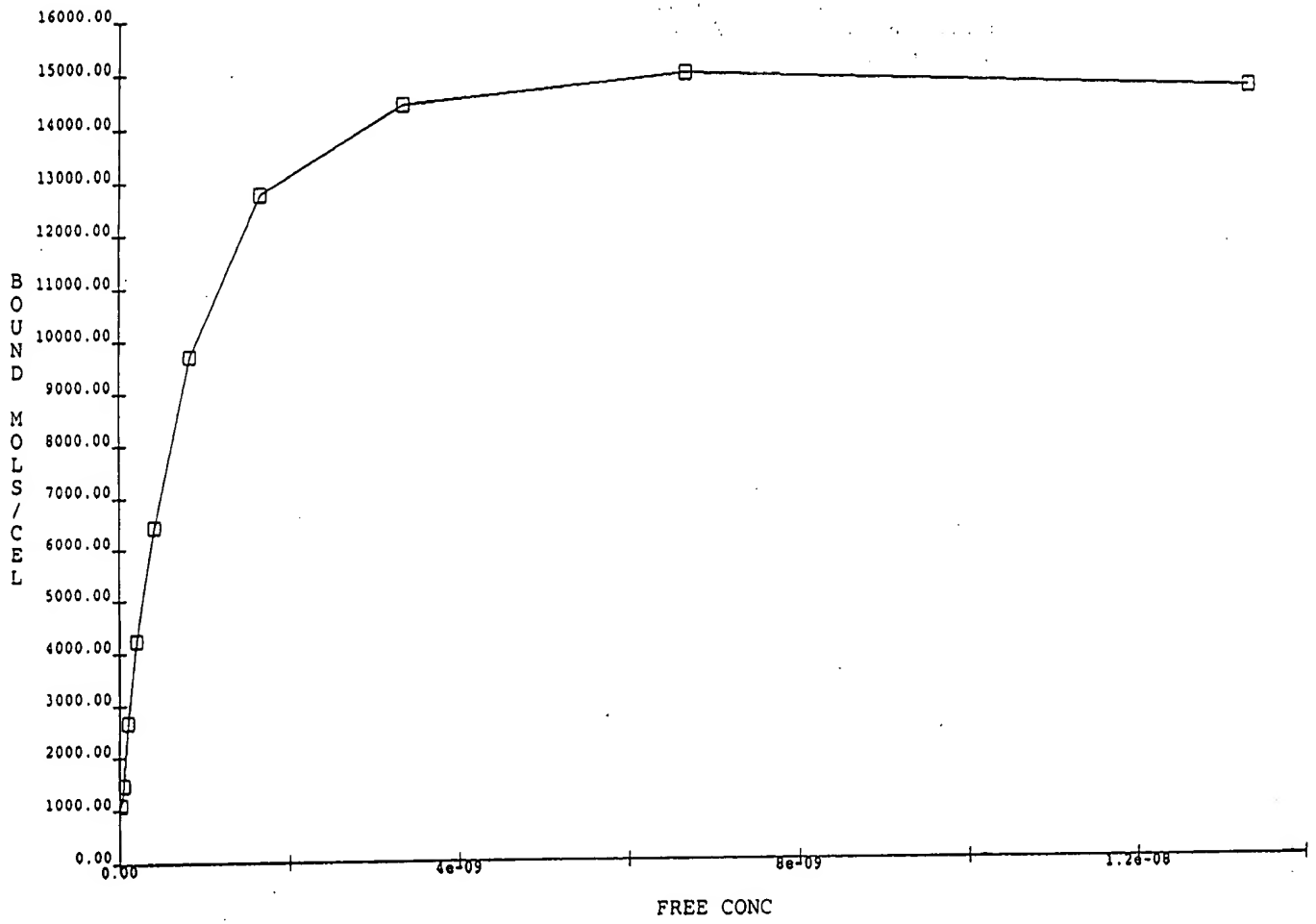

Figure 5A

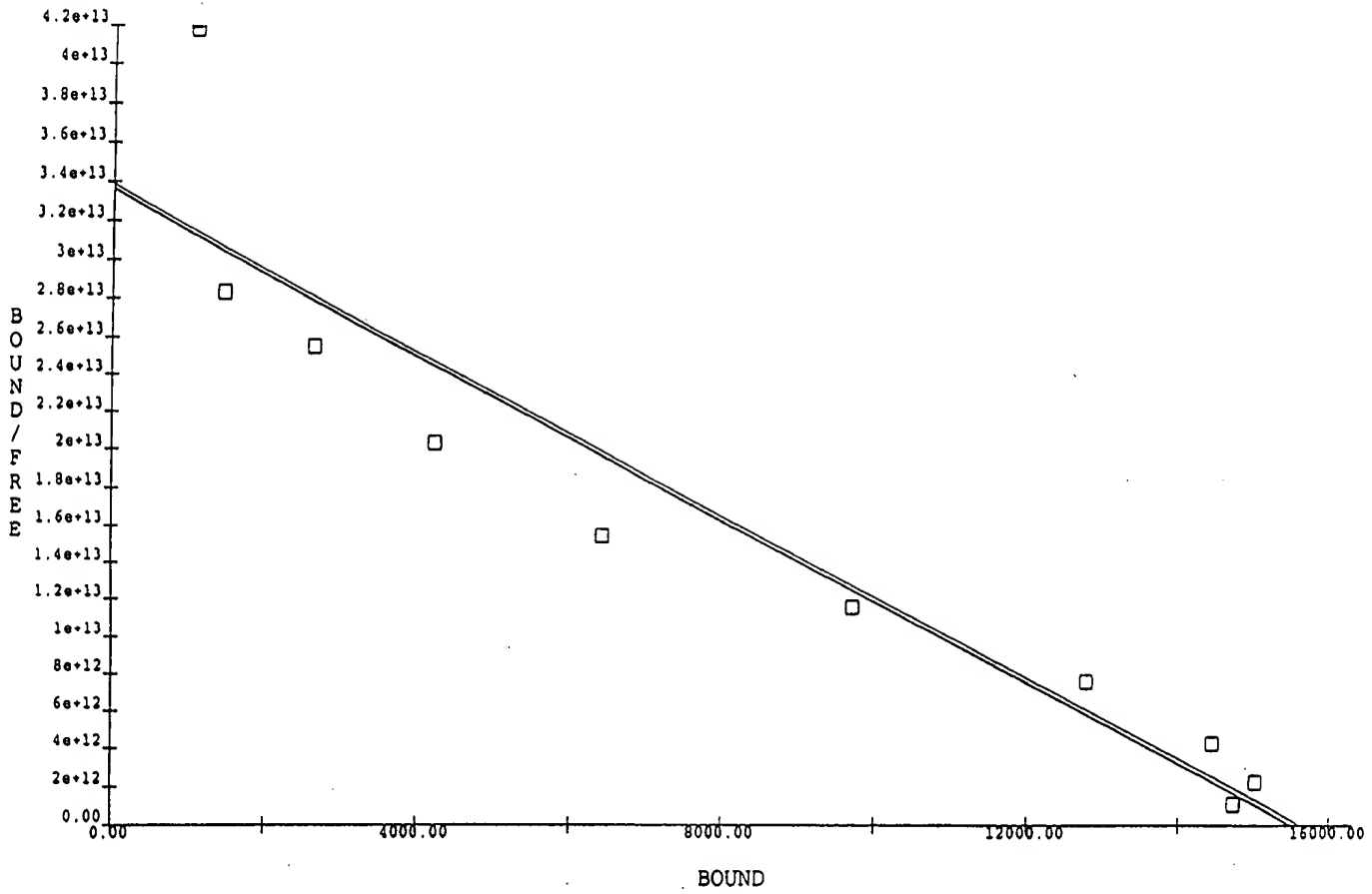
4.2e+13
4e+13
3.8e+13
3.6e+13
3.4e+13
3.2e+13
3e+13
2.8e+13
2.6e+13
2.4e+13
2.2e+13
2e+13
1.8e+13
1.6e+13
1.4e+13
1.2e+13
1e+13
8e+12
6e+12
4e+12
2e+12
0.00
BOUND/FREE
0.00
4000.00
8000.00
12000.00
16000.00
BOUND

Figure 5B

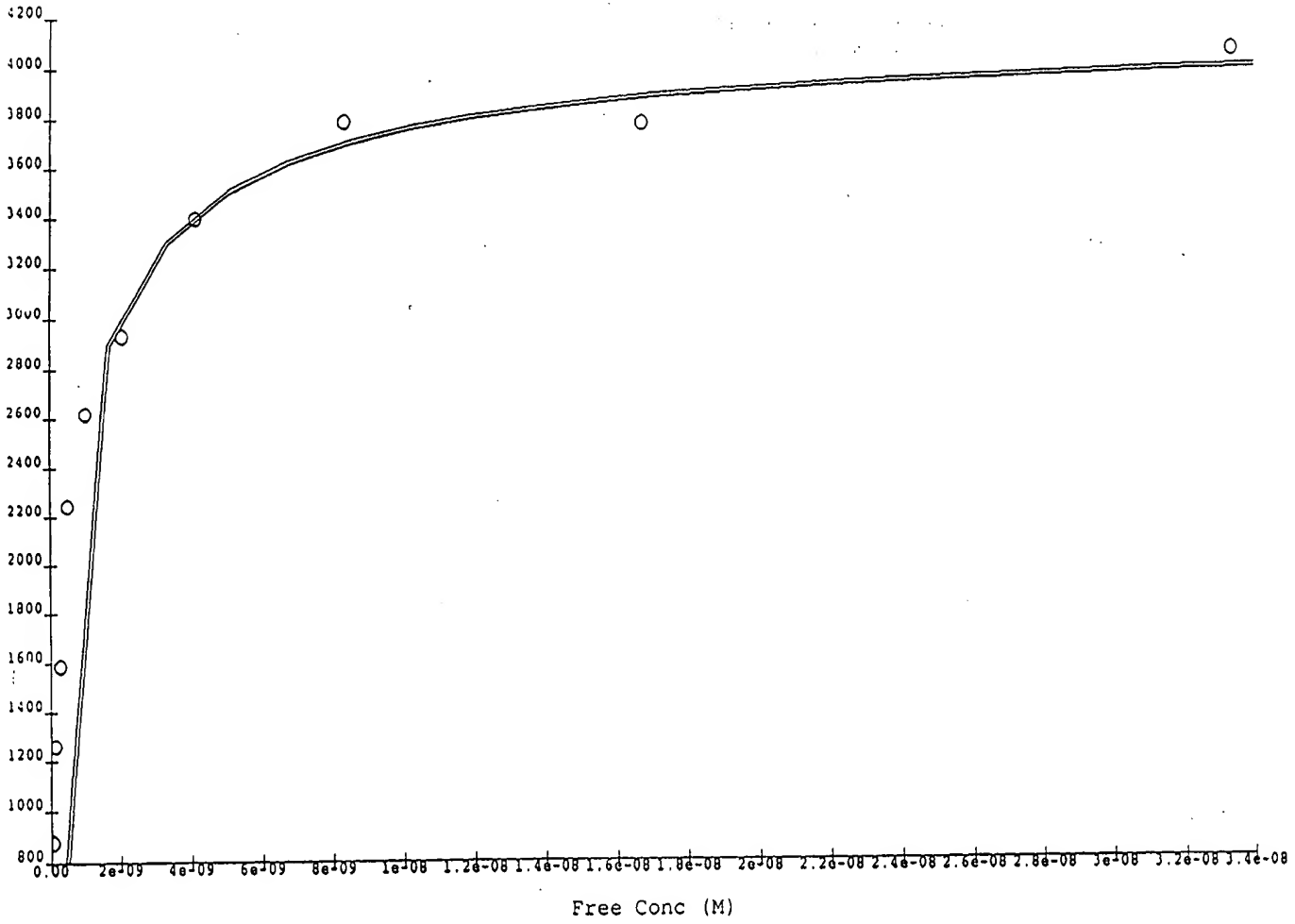
4200
4000
3800
3600
3400
3200
3000
2800
2600
2400
2200
2000
1800
1600
1400
1200
1000
800
0.00
2e-09
4e-09
6e-09
8e-09
1e-08
1.2e-08
1.4e-08
1.6e-08
1.8e-08
2e-08
2.2e-08
2.4e-08
2.6e-08
2.8e-08
3e-08
3.2e-08
3.4e-08
Free Conc (M)

Figure 6A

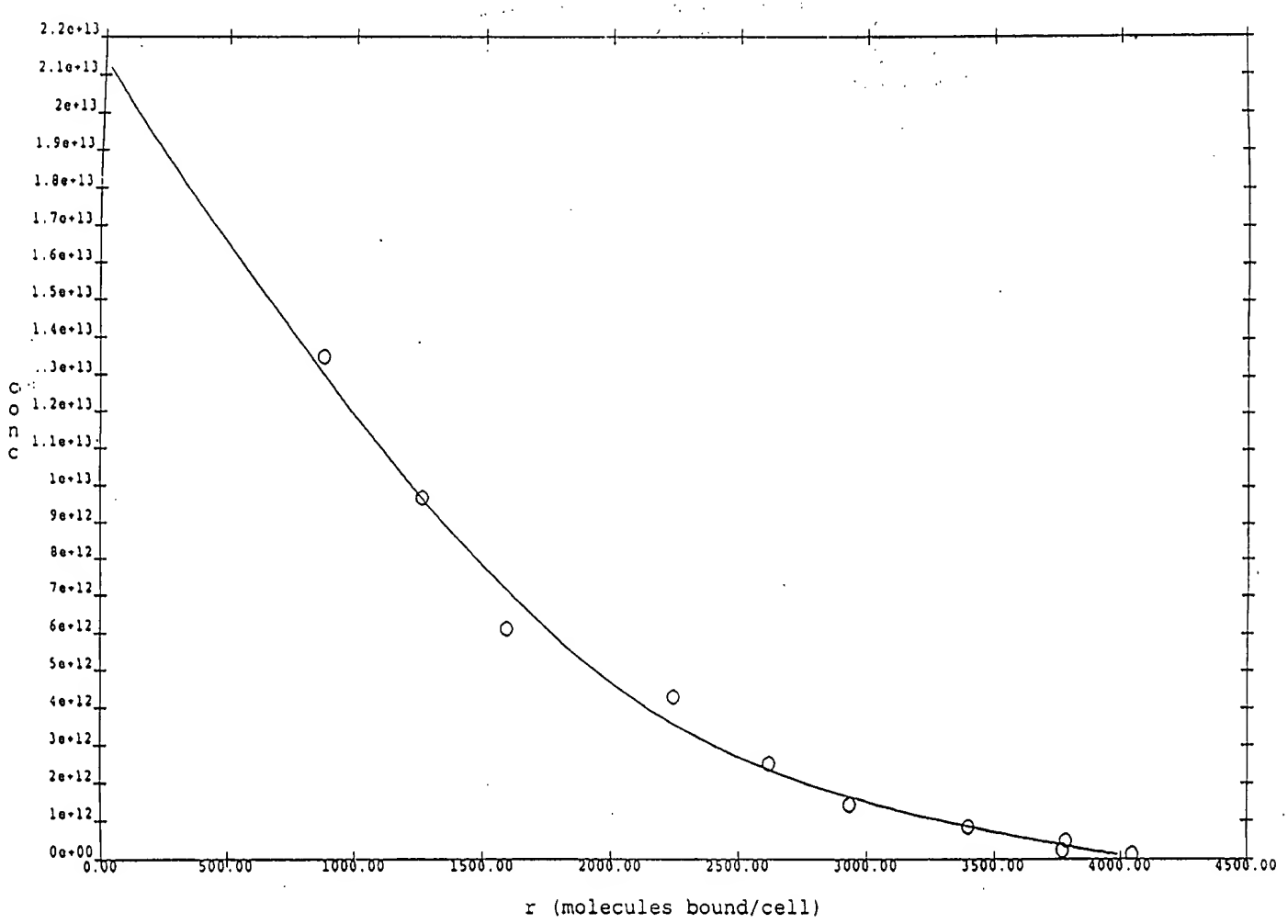
2.2e+13
2.1e+13
2e+13
1.9e+13
1.8e+13
1.7e+13
1.6e+13
1.5e+13
1.4e+13
1.3e+13
1.2e+13
1.1e+13
1e+13
9e+12
8e+12
7e+12
6e+12
5e+12
4e+12
3e+12
2e+12
1e+12
0e+00
conc
0.00
500.00
1000.00
1500.00
2000.00
2500.00
3000.00
3500.00
4000.00
4500.00
r (molecules bound/cell)

Figure 6B